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TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,495B

DATE: 11/21/2002

TIME: 11:00:29

Input Set : A:\-7-2-1.app

Output Set: N:\CRF4\11212002\I721495B.raw

#15

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3 <110> APPLICANT: Gosling, Jennifa
4      Dairaghi, Daniel J.
5      Hanley, Michael
6      Miao, Zhenhua
7      Talbot, Dale
8      Schall, Thomas J.
9      ChemoCentryx, Inc.
11 <120> TITLE OF INVENTION: Chemokine Receptor
13 <130> FILE REFERENCE: 019934-0007210US
15 <140> CURRENT APPLICATION NUMBER: US 09/721,495B
16 <141> CURRENT FILING DATE: 2000-11-21
18 <150> PRIOR APPLICATION NUMBER: US 60/159,015
19 <151> PRIOR FILING DATE: 1999-10-12
21 <150> PRIOR APPLICATION NUMBER: US 60/159,210
22 <151> PRIOR FILING DATE: 1999-10-13
24 <150> PRIOR APPLICATION NUMBER: US 60/172,979
25 <151> PRIOR FILING DATE: 1999-12-20
27 <150> PRIOR APPLICATION NUMBER: US 60/173,388
28 <151> PRIOR FILING DATE: 1999-12-28
30 <150> PRIOR APPLICATION NUMBER: US 60/186,626
31 <151> PRIOR FILING DATE: 2000-03-03
33 <150> PRIOR APPLICATION NUMBER: US 09/686,019
34 <151> PRIOR FILING DATE: 2000-10-10
36 <160> NUMBER OF SEQ ID NOS: 14
38 <170> SOFTWARE: PatentIn Ver. 2.1
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42 <212> TYPE: DNA
43 <213> ORGANISM: Homo sapiens
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46 <221> NAME/KEY: CDS
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55   1               5               10               15
57 gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc      96
58 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
59           20           25           30
61 aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc     144
62 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu

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63	35	40	45	
65	aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192		
66	Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala			
67	50	55	60	
69	att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240		
70	Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile			
71	65	70	75	80
73	ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288		
74	Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe			
75	85	90	95	
77	tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336		
78	Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys			
79	100	105	110	
81	aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384		
82	Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln			
83	115	120	125	
85	ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc	432		
86	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val			
87	130	135	140	
89	ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt	480		
90	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys			
91	145	150	155	160
93	gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528		
94	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr			
95	165	170	175	
97	aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576		
98	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu			
99	180	185	190	
101	gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624		
102	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly			
103	195	200	205	
105	ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca	672		
106	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala			
107	210	215	220	
109	agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa	720		
110	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys			
111	225	230	235	240
113	gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat	768		
114	Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr			
115	245	250	255	
117	aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc	816		
118	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile			
119	260	265	270	
121	acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca	864		
122	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr			
123	275	280	285	
125	gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt	912		
126	Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val			
127	290	295	300	

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129 ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa 960
130 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
131 305 310 315 320
133 tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt 1008
134 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
135 325 330 335
137 gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa 1053
138 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
139 340 345 350
141 aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgctttcc cctcaaataa 1113
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148 <212> TYPE: PRT
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151 <220> FEATURE:
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154 <400> SEQUENCE: 2
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156 1 5 10 15
157 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
158 20 25 30
159 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
160 35 40 45
161 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
162 50 55 60
163 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
164 65 70 75 80
165 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
166 85 90 95
167 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
168 100 105 110
169 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
170 115 120 125
171 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
172 130 135 140
173 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
174 145 150 155 160
175 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
176 165 170 175
177 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
178 180 185 190
179 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
180 195 200 205
181 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
182 210 215 220
183 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
184 225 230 235 240
185 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr

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186          245          250          255
187 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
188          260          265          270
189 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
190          275          280          285
191 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
192          290          295          300
193 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
194 305          310          315          320
195 Tyr Gly Ser Trp Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
196          325          330          335
197 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
198          340          345          350
201 <210> SEQ ID NO: 3
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203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <223> OTHER INFORMATION: chemokine receptor CCX CKR (variant)
209 <400> SEQUENCE: 3
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211 actgatgact acagtcagta tgaactgac tgtatcaaag aagatgtcag agaatttgcc 120
212 aaagttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
213 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
214 ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcctttttg ggctgttaat 300
215 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
216 ctaaaactttg tctctggaat gcagtttctg gcttgtatca gcatagacag atatgtggca 420
217 gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480
218 gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaataac 540
219 aatgttaggt gcattcccat tttccccgc aacttaggaa catcaatgaa agcattgatt 600
220 caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgctac 660
221 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
222 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
223 ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
224 atggacatcg ccatccaagt cacagaaagc atcgactctt ttcacagctg cctcaaccca 900
225 atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960
226 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
227 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
228 gatacatatg aatgatgctt tcccctcaaa taaaacatct gccttattct gaaaaaaaaa 1140
229 aaaaaam 1147
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234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
240 <400> SEQUENCE: 4
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257 <211> LENGTH: 369
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <223> OTHER INFORMATION: chemokine receptor CCR9
264 <400> SEQUENCE: 6
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266 1 5 10 15
267 Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr Val Asn Phe Asn
268 20 25 30
269 Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser
270 35 40 45
271 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
272 50 55 60
273 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
274 65 70 75 80
275 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
276 85 90 95
277 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala Asp Gln Trp
278 100 105 110
279 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
280 115 120 125
281 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
282 130 135 140
283 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
284 145 150 155 160
285 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
286 165 170 175
287 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
288 180 185 190
289 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
290 195 200 205
291 Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
292 210 215 220
293 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
294 225 230 235 240
295 Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr
296 245 250 255
297 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
298 260 265 270
299 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn

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VERIFICATION SUMMARY

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